



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:23 AM UTC

PDB ID : 5D0V / pdb_00005d0v
Title : Yeast 20S proteasome beta5-T1C mutant in complex with Carfilzomib
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-08-03
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

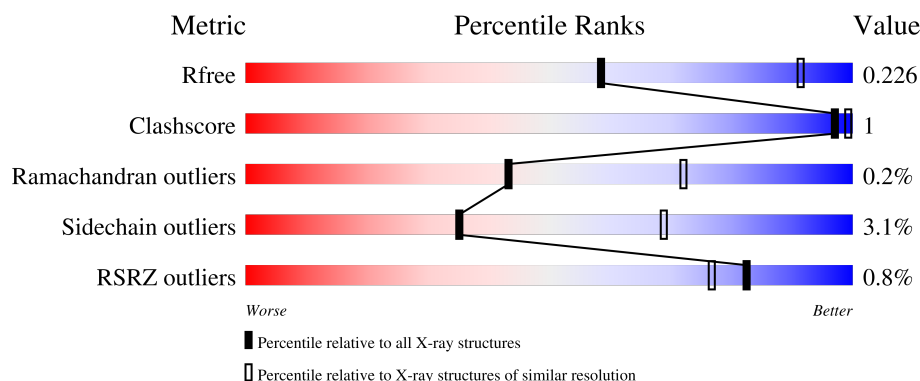
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

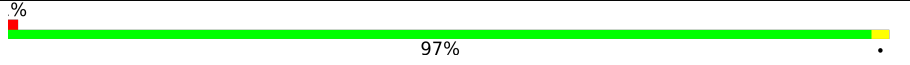
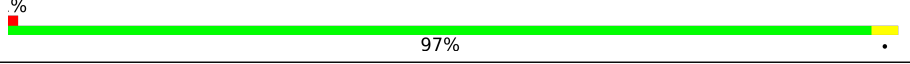
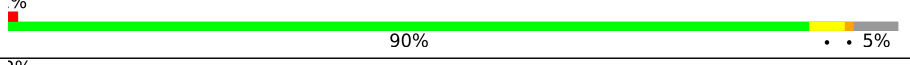
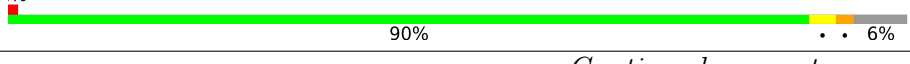
The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	
1	O	250	
2	B	258	
2	P	258	
3	C	254	

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	218	
11	Y	218	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 49848 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

- Molecule 6 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1906	1214	320	364	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	218	Total	C	N	O	S	0	0	0
			1687	1073	289	317	8			
11	Y	212	Total	C	N	O	S	0	0	0
			1643	1044	280	311	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	CYS	THR	engineered mutation	UNP P30656
Y	1	CYS	THR	engineered mutation	UNP P30656

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

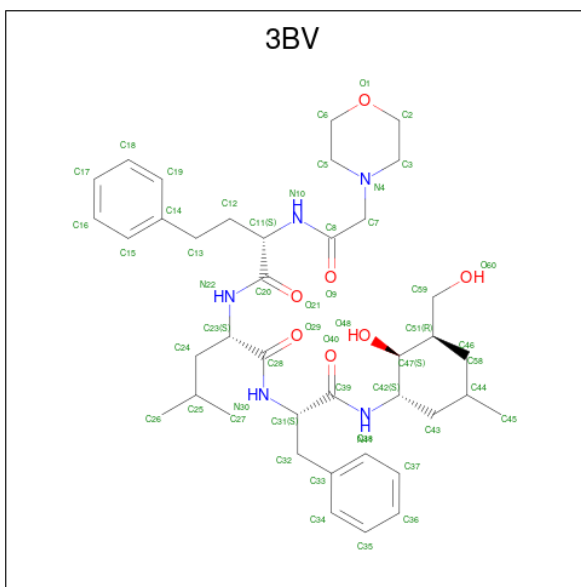
- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	G	1	Total Mg 1 1	0	0
15	H	1	Total Mg 1 1	0	0
15	I	2	Total Mg 2 2	0	0
15	K	1	Total Mg 1 1	0	0
15	L	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

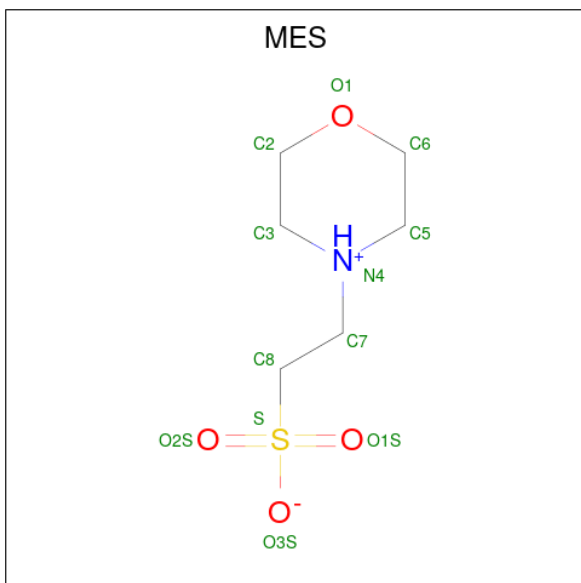
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	N	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0
16	b	1	Total Cl 1 1	0	0

- Molecule 17 is N-{(2S)-2-[(morpholin-4-ylacetyl)amino]-4-phenylbutanoyl}-L-leucyl-N-[(2R,3S,4S)-1,3-dihydroxy-2,6-dimethylheptan-4-yl]-L-phenylalaninamide (CCD ID: 3BV) (formula: C₄₀H₆₁N₅O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	H	1	Total	C	N	O	0	0
			52	40	5	7		
17	N	1	Total	C	N	O	0	0
			52	40	5	7		
17	V	1	Total	C	N	O	0	0
			52	40	5	7		
17	b	1	Total	C	N	O	0	0
			52	40	5	7		

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	V	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	9	Total	O	0	0
			9	9		
19	B	15	Total	O	0	0
			15	15		
19	C	4	Total	O	0	0
			4	4		
19	D	5	Total	O	0	0
			5	5		
19	E	5	Total	O	0	0
			5	5		
19	F	8	Total	O	0	0
			8	8		
19	G	11	Total	O	0	0
			11	11		
19	H	12	Total	O	0	0
			12	12		
19	I	6	Total	O	0	0
			6	6		
19	J	18	Total	O	0	0
			18	18		
19	K	10	Total	O	0	0
			10	10		
19	L	14	Total	O	0	0
			14	14		
19	M	11	Total	O	0	0
			11	11		
19	N	8	Total	O	0	0
			8	8		
19	O	5	Total	O	0	0
			5	5		
19	P	11	Total	O	0	0
			11	11		
19	Q	5	Total	O	0	0
			5	5		
19	R	6	Total	O	0	0
			6	6		

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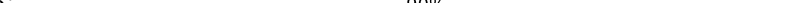
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	S	4	Total 4	O 4	0	0
19	T	10	Total 10	O 10	0	0
19	U	5	Total 5	O 5	0	0
19	V	18	Total 18	O 18	0	0
19	W	5	Total 5	O 5	0	0
19	X	10	Total 10	O 10	0	0
19	Y	8	Total 8	O 8	0	0
19	Z	18	Total 18	O 18	0	0
19	a	14	Total 14	O 14	0	0
19	b	12	Total 12	O 12	0	0

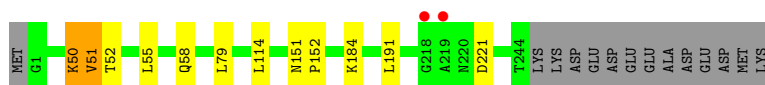
- Molecule 1: Proteasome subunit alpha type-2

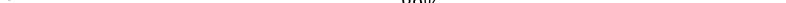


- Chain O:

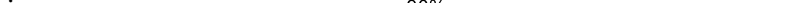


- Chain B:  90% . . 5%



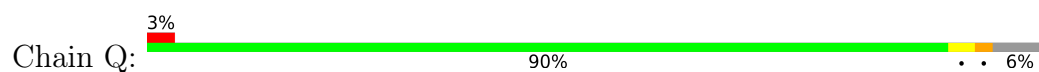
- Chain P:  2% 89% 5% • 5%



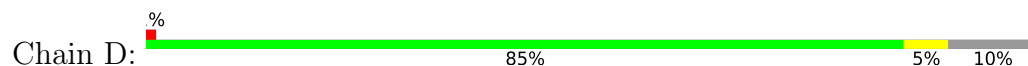
- Chain C:  90% 6%



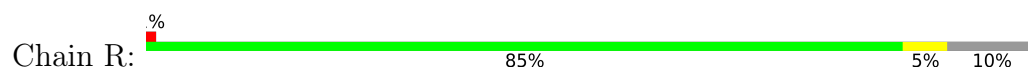
- 
- WORLD WIDE
PDB
PROTEIN DATA BANK



- Molecule 4: Proteasome subunit alpha type-5



- Molecule 4: Proteasome subunit alpha type-5



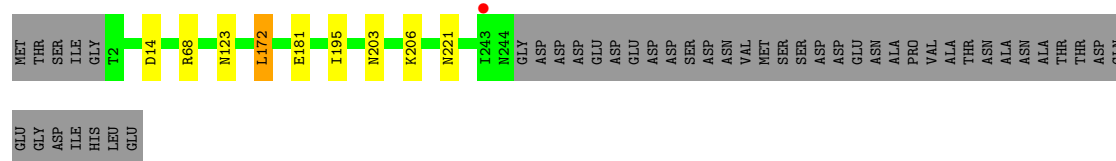
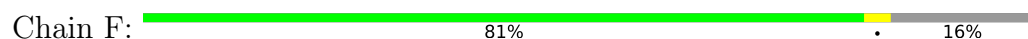
- Molecule 5: Proteasome subunit alpha type-6



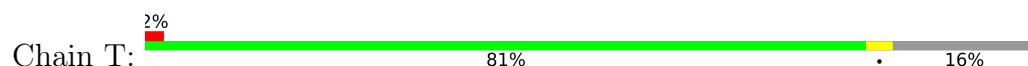
- Molecule 5: Proteasome subunit alpha type-6

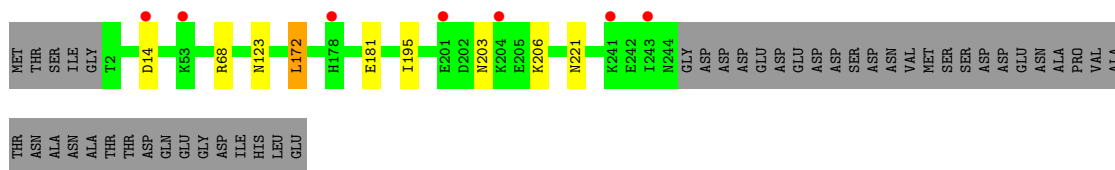


- Molecule 6: Probable proteasome subunit alpha type-7



- Molecule 6: Probable proteasome subunit alpha type-7





- Molecule 7: Proteasome subunit alpha type-1

Chain G: 91% 5% .



- Molecule 7: Proteasome subunit alpha type-1

Chain U: 91% 5% .



- Molecule 8: Proteasome subunit beta type-2

Chain H: 92% . .



- Molecule 8: Proteasome subunit beta type-2

Chain V: 92% . .



- Molecule 9: Proteasome subunit beta type-3

Chain I: 95% 5%

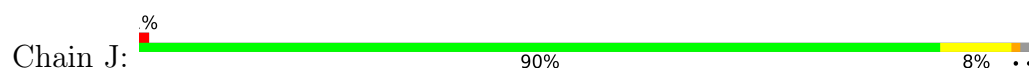


- Molecule 9: Proteasome subunit beta type-3

Chain W: 94% 5%



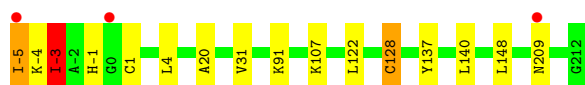
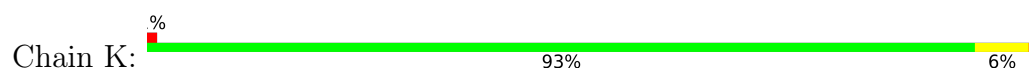
- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



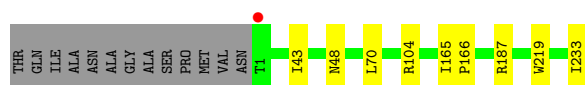
- Molecule 12: Proteasome subunit beta type-6



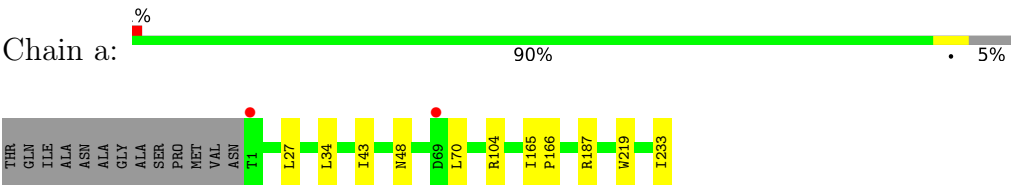
- Molecule 12: Proteasome subunit beta type-6



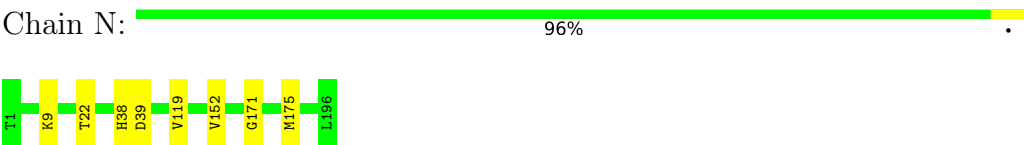
- Molecule 13: Proteasome subunit beta type-7



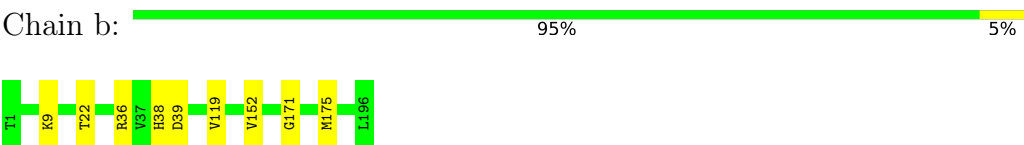
● Molecule 13: Proteasome subunit beta type-7



● Molecule 14: Proteasome subunit beta type-1



● Molecule 14: Proteasome subunit beta type-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.17Å 299.94Å 144.94Å 90.00° 112.56° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90 15.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (15.00-2.90) 97.0 (15.00-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.193 , 0.220 0.199 , 0.226	Depositor DCC
R_{free} test set	11382 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	61.8	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49848	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3BV, MG, MES, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.40	0/1952	0.69	0/2642
1	O	0.39	0/1952	0.69	0/2642
2	B	0.39	0/1934	0.67	0/2618
2	P	0.39	0/1934	0.67	0/2618
3	C	0.40	0/1910	0.70	1/2586 (0.0%)
3	Q	0.40	0/1910	0.70	1/2586 (0.0%)
4	D	0.38	0/1837	0.65	0/2475
4	R	0.38	0/1837	0.64	0/2475
5	E	0.39	0/1800	0.66	0/2433
5	S	0.39	0/1800	0.66	0/2433
6	F	0.39	0/1932	0.69	0/2609
6	T	0.39	0/1932	0.70	0/2609
7	G	0.38	0/1945	0.66	0/2634
7	U	0.38	0/1944	0.66	0/2632
8	H	0.38	0/1715	0.65	0/2326
8	V	0.39	0/1715	0.64	0/2326
9	I	0.38	0/1611	0.67	0/2174
9	W	0.37	0/1611	0.67	0/2174
10	J	0.38	0/1589	0.67	0/2142
10	X	0.38	0/1589	0.67	0/2142
11	K	0.38	0/1724	0.66	0/2329
11	Y	0.37	0/1680	0.65	0/2272
12	L	0.38	0/1795	0.66	0/2420
12	Z	0.38	0/1795	0.66	0/2420
13	M	0.39	0/1855	0.67	0/2514
13	a	0.39	0/1855	0.67	0/2514
14	N	0.37	0/1541	0.68	0/2087
14	b	0.37	0/1541	0.68	0/2087
All	All	0.39	0/50235	0.67	2/67919 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	201	VAL	N-CA-C	5.93	116.06	110.30
3	C	201	VAL	N-CA-C	5.88	116.00	110.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	2	0
1	O	1915	0	1929	4	0
2	B	1904	0	1904	2	0
2	P	1904	0	1904	4	0
3	C	1881	0	1895	4	0
3	Q	1881	0	1895	5	0
4	D	1813	0	1797	2	0
4	R	1813	0	1797	2	0
5	E	1773	0	1775	3	0
5	S	1773	0	1775	3	0
6	F	1892	0	1883	1	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	3	0
7	U	1906	0	1901	3	0
8	H	1684	0	1686	3	0
8	V	1684	0	1686	3	0
9	I	1581	0	1574	4	0
9	W	1581	0	1574	5	0
10	J	1561	0	1569	10	0
10	X	1561	0	1569	7	0
11	K	1687	0	1645	8	0
11	Y	1643	0	1593	2	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	4	0
13	M	1824	0	1832	2	0
13	a	1824	0	1832	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	N	1512	0	1478	3	0
14	b	1512	0	1478	4	0
15	G	1	0	0	0	0
15	H	1	0	0	0	0
15	I	2	0	0	0	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	N	1	0	0	0	0
16	U	1	0	0	0	0
16	b	1	0	0	0	0
17	H	52	0	59	3	0
17	N	52	0	59	1	0
17	V	52	0	59	3	0
17	b	52	0	59	1	0
18	H	12	0	13	0	0
18	V	12	0	13	0	0
19	A	9	0	0	0	0
19	B	15	0	0	0	0
19	C	4	0	0	0	0
19	D	5	0	0	0	0
19	E	5	0	0	0	0
19	F	8	0	0	0	0
19	G	11	0	0	0	0
19	H	12	0	0	0	0
19	I	6	0	0	0	0
19	J	18	0	0	0	0
19	K	10	0	0	1	0
19	L	14	0	0	0	0
19	M	11	0	0	0	0
19	N	8	0	0	0	0
19	O	5	0	0	0	0
19	P	11	0	0	0	0
19	Q	5	0	0	0	0
19	R	6	0	0	0	0
19	S	4	0	0	0	0
19	T	10	0	0	0	0
19	U	5	0	0	0	0
19	V	18	0	0	0	0
19	W	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	X	10	0	0	0	0
19	Y	8	0	0	0	0
19	Z	18	0	0	0	0
19	a	14	0	0	0	0
19	b	12	0	0	1	0
All	All	49848	0	49368	92	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (92) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.83	0.61
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.83	0.60
10:J:91:SER:HG	10:J:98:TYR:H	1.50	0.59
14:b:152:VAL:HA	14:b:175:MET:HE1	1.88	0.56
8:H:168:GLY:O	17:H:301:3BV:H57	2.07	0.55
7:G:23:PHE:O	7:G:26:THR:HB	2.07	0.55
8:V:168:GLY:O	17:V:301:3BV:H57	2.06	0.55
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.42	0.55
14:N:152:VAL:HA	14:N:175:MET:HE1	1.88	0.54
14:b:36:ARG:NH1	19:b:301:HOH:O	2.40	0.54
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.43	0.54
7:U:23:PHE:O	7:U:26:THR:HB	2.08	0.52
11:K:107:LYS:NZ	19:K:401:HOH:O	2.43	0.52
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.58	0.51
3:C:201:VAL:O	3:C:202:GLN:CB	2.58	0.51
11:K:-5:ILE:HG22	11:K:-4:LYS:H	1.77	0.50
11:K:-4:LYS:O	11:K:-3:ILE:HG12	2.12	0.49
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.94	0.49
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.95	0.49
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.95	0.48
2:P:50:LYS:O	2:P:51:VAL:C	2.57	0.48
17:b:201:3BV:O48	17:b:201:3BV:O60	2.23	0.48
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.96	0.47
2:B:50:LYS:O	2:B:51:VAL:C	2.58	0.46
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.97	0.46
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.97	0.46
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.99	0.45
17:N:201:3BV:O60	17:N:201:3BV:O48	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:49:ALA:HB2	17:V:301:3BV:H52	1.98	0.45
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.46	0.45
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.99	0.45
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.47	0.45
8:H:49:ALA:HB2	17:H:301:3BV:H52	1.97	0.45
10:X:36:ARG:NH1	10:X:58:GLU:OE2	2.49	0.45
14:N:171:GLY:HA2	13:a:219:TRP:CH2	2.52	0.44
8:H:104:ASP:HB2	8:H:105:PRO:HD2	2.00	0.44
9:I:10:ILE:HG21	9:I:141:ALA:HB3	2.00	0.44
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.99	0.44
1:A:115:ALA:HB1	1:A:154:GLY:O	2.18	0.44
1:O:115:ALA:HB1	1:O:154:GLY:O	2.18	0.44
10:J:36:ARG:NH1	10:J:58:GLU:OE2	2.50	0.43
9:W:36:SER:HB2	10:X:126:VAL:HG11	2.00	0.43
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.99	0.43
3:C:201:VAL:HG13	3:C:202:GLN:N	2.33	0.43
12:L:8:ASN:HA	12:L:30:ILE:O	2.19	0.43
9:I:9:GLY:HA3	9:I:41:LYS:HE2	2.00	0.43
9:W:9:GLY:HA3	9:W:41:LYS:HE2	2.00	0.43
10:X:3:ILE:HD12	10:X:176:PHE:CG	2.54	0.43
5:S:77:ALA:N	5:S:78:PRO:CD	2.82	0.43
4:D:113:LEU:HD12	5:E:78:PRO:HB2	2.01	0.42
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.33	0.42
8:V:104:ASP:HB2	8:V:105:PRO:HD2	2.00	0.42
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.19	0.42
11:K:209:ASN:O	9:W:38:LYS:NZ	2.48	0.42
5:E:77:ALA:N	5:E:78:PRO:CD	2.83	0.42
10:J:174:MET:HA	10:X:174:MET:HA	2.01	0.42
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.50	0.42
10:J:21:VAL:HG11	11:K:122:LEU:HD11	2.02	0.42
13:M:219:TRP:CH2	14:b:171:GLY:HA2	2.54	0.42
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.85	0.42
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	2.02	0.42
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.50	0.42
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.55	0.42
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.35	0.41
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.50	0.41
9:I:20:VAL:HG13	9:I:118:PRO:HB3	2.02	0.41
10:J:3:ILE:HD12	10:J:176:PHE:CG	2.55	0.41
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.48	0.41
1:O:119:GLN:O	1:O:122:THR:HB	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:20:VAL:HG13	9:W:118:PRO:HB3	2.02	0.41
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.85	0.41
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.85	0.41
13:a:165:ILE:HB	13:a:166:PRO:HD3	2.03	0.41
14:N:38:HIS:O	14:N:39:ASP:C	2.63	0.41
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.41
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.51	0.41
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.48	0.41
17:H:301:3BV:H32	17:H:301:3BV:H29	1.96	0.41
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.56	0.41
3:Q:161:THR:HG21	3:Q:169:VAL:HG13	2.03	0.41
1:A:119:GLN:O	1:A:122:THR:HB	2.20	0.41
10:J:50:ALA:O	11:K:91:LYS:NZ	2.54	0.41
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.02	0.41
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.55	0.41
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.56	0.41
11:K:128:CYS:HB2	11:K:137:TYR:CZ	2.56	0.41
12:L:147:MET:N	12:L:148:PRO:HD2	2.36	0.41
14:b:38:HIS:O	14:b:39:ASP:C	2.63	0.41
10:J:3:ILE:HD12	10:J:176:PHE:CD2	2.57	0.40
17:V:301:3BV:N41	17:V:301:3BV:H60	2.37	0.40
13:a:27:LEU:HD21	13:a:34:LEU:HD22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	16	44
2	P	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	16	44
3	C	238/254 (94%)	229 (96%)	7 (3%)	2 (1%)	16	44
3	Q	238/254 (94%)	229 (96%)	7 (3%)	2 (1%)	16	44
4	D	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
4	R	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
5	E	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
5	S	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
6	F	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
7	U	239/252 (95%)	234 (98%)	5 (2%)	0	100	100
8	H	220/232 (95%)	216 (98%)	4 (2%)	0	100	100
8	V	220/232 (95%)	216 (98%)	4 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	24	54
10	X	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	24	54
11	K	214/218 (98%)	210 (98%)	3 (1%)	1 (0%)	24	54
11	Y	210/218 (96%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
13	M	231/246 (94%)	222 (96%)	9 (4%)	0	100	100
13	a	231/246 (94%)	222 (96%)	9 (4%)	0	100	100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
All	All	6280/6626 (95%)	6104 (97%)	165 (3%)	11 (0%)	43	72

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN

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Mol	Chain	Res	Type
2	P	51	VAL
3	Q	202	GLN
11	K	-3	ILE
3	C	205	ALA
3	Q	205	ALA
2	B	221	ASP
2	P	221	ASP
10	J	2	ASP
10	X	2	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	205 (98%)	4 (2%)	50	79
1	O	209/209 (100%)	205 (98%)	4 (2%)	50	79
2	B	203/216 (94%)	195 (96%)	8 (4%)	28	63
2	P	203/216 (94%)	195 (96%)	8 (4%)	28	63
3	C	212/226 (94%)	205 (97%)	7 (3%)	33	67
3	Q	212/226 (94%)	205 (97%)	7 (3%)	33	67
4	D	194/215 (90%)	183 (94%)	11 (6%)	18	49
4	R	194/215 (90%)	183 (94%)	11 (6%)	18	49
5	E	190/193 (98%)	184 (97%)	6 (3%)	34	68
5	S	190/193 (98%)	185 (97%)	5 (3%)	40	73
6	F	201/239 (84%)	193 (96%)	8 (4%)	28	62
6	T	201/239 (84%)	193 (96%)	8 (4%)	28	62
7	G	206/210 (98%)	200 (97%)	6 (3%)	37	71
7	U	206/210 (98%)	200 (97%)	6 (3%)	37	71
8	H	181/190 (95%)	177 (98%)	4 (2%)	45	77
8	V	181/190 (95%)	177 (98%)	4 (2%)	45	77
9	I	172/173 (99%)	169 (98%)	3 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	W	172/173 (99%)	169 (98%)	3 (2%)	53	82
10	J	173/175 (99%)	169 (98%)	4 (2%)	44	76
10	X	173/175 (99%)	169 (98%)	4 (2%)	44	76
11	K	173/173 (100%)	165 (95%)	8 (5%)	24	57
11	Y	169/173 (98%)	164 (97%)	5 (3%)	36	70
12	L	185/185 (100%)	178 (96%)	7 (4%)	29	64
12	Z	185/185 (100%)	178 (96%)	7 (4%)	29	64
13	M	199/208 (96%)	193 (97%)	6 (3%)	36	70
13	a	199/208 (96%)	193 (97%)	6 (3%)	36	70
14	N	162/162 (100%)	159 (98%)	3 (2%)	50	79
14	b	162/162 (100%)	159 (98%)	3 (2%)	50	79
All	All	5316/5548 (96%)	5150 (97%)	166 (3%)	35	69

All (166) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	61	LEU
1	A	122	THR
1	A	157	PHE
2	B	50	LYS
2	B	52	THR
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	114	LEU
2	B	184	LYS
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	203	THR
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU

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Mol	Chain	Res	Type
4	D	99	ILE
4	D	125	LEU
4	D	176	LEU
4	D	193	LEU
4	D	197	LYS
4	D	214	ILE
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	71	LEU
5	E	188	LEU
6	F	14	ASP
6	F	68	ARG
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	221	ASN
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
10	J	23	ARG
10	J	75	LEU
10	J	144	LEU
10	J	174	MET
11	K	-5	ILE
11	K	-3	ILE
11	K	-1	HIS

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Mol	Chain	Res	Type
11	K	1	CYS
11	K	4	LEU
11	K	128	CYS
11	K	140	LEU
11	K	148	LEU
12	L	1	GLN
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	187	ARG
13	M	233	ILE
14	N	9	LYS
14	N	22	THR
14	N	119	VAL
1	O	17	LYS
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
2	P	50	LYS
2	P	52	THR
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	114	LEU
2	P	184	LYS
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	203	THR
4	R	20	LEU
4	R	40	LEU

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Mol	Chain	Res	Type
4	R	51	LEU
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	197	LYS
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	54	GLU
5	S	71	LEU
5	S	188	LEU
6	T	14	ASP
6	T	68	ARG
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	221	ASN
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
10	X	23	ARG
10	X	75	LEU
10	X	144	LEU
10	X	174	MET
11	Y	1	CYS
11	Y	4	LEU
11	Y	128	CYS

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Mol	Chain	Res	Type
11	Y	140	LEU
11	Y	148	LEU
12	Z	1	GLN
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	187	ARG
13	a	233	ILE
14	b	9	LYS
14	b	22	THR
14	b	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	58	GLN
2	B	119	GLN
2	B	123	GLN
2	B	232	GLN
3	C	38	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	233	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	106	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN

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Mol	Chain	Res	Type
5	E	120	GLN
5	E	151	ASN
5	E	165	GLN
5	E	184	ASN
6	F	86	ASN
6	F	123	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	175	ASN
8	H	30	ASN
8	H	66	HIS
8	H	86	HIS
8	H	189	ASN
9	I	44	HIS
9	I	63	ASN
9	I	88	GLN
10	J	55	GLN
10	J	63	ASN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	208	ASN
12	L	153	GLN
13	M	26	ASN
13	M	102	GLN
14	N	38	HIS
14	N	141	ASN
1	O	30	GLN
1	O	149	GLN
2	P	58	GLN
2	P	232	GLN
3	Q	38	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	233	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN

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Mol	Chain	Res	Type
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	165	GLN
5	S	184	ASN
6	T	86	ASN
6	T	123	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	175	ASN
8	V	30	ASN
8	V	66	HIS
8	V	86	HIS
8	V	172	ASN
8	V	189	ASN
8	V	194	ASN
8	V	200	GLN
9	W	44	HIS
9	W	63	ASN
9	W	88	GLN
10	X	55	GLN
10	X	63	ASN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	70	ASN
12	Z	153	GLN
13	a	102	GLN
13	a	149	HIS
14	b	141	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	MES	H	302	-	12,12,12	2.22	1 (8%)	15,16,16	1.15	1 (6%)
17	3BV	b	201	14	54,54,54	1.32	4 (7%)	68,71,71	1.48	9 (13%)
17	3BV	H	301	8	54,54,54	1.09	3 (5%)	68,71,71	1.53	10 (14%)
18	MES	V	302	-	12,12,12	2.25	1 (8%)	15,16,16	1.14	2 (13%)
17	3BV	V	301	8	54,54,54	1.09	3 (5%)	68,71,71	1.53	10 (14%)
17	3BV	N	201	14	54,54,54	1.33	4 (7%)	68,71,71	1.46	9 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	MES	H	302	-	-	5/6/14/14	0/1/1/1
17	3BV	b	201	14	-	14/59/67/67	0/3/3/3
17	3BV	H	301	8	-	4/59/67/67	0/3/3/3
18	MES	V	302	-	-	2/6/14/14	0/1/1/1
17	3BV	V	301	8	-	4/59/67/67	0/3/3/3
17	3BV	N	201	14	-	14/59/67/67	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	V	302	MES	C8-S	-7.45	1.67	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	H	302	MES	C8-S	-7.38	1.67	1.77
17	b	201	3BV	C51-C47	5.64	1.63	1.53
17	N	201	3BV	C51-C47	5.63	1.63	1.53
17	H	301	3BV	C32-C33	-4.56	1.40	1.51
17	V	301	3BV	C32-C33	-4.52	1.40	1.51
17	b	201	3BV	C32-C33	-4.44	1.40	1.51
17	N	201	3BV	C32-C33	-4.43	1.40	1.51
17	b	201	3BV	C13-C14	-3.70	1.41	1.51
17	N	201	3BV	C13-C14	-3.67	1.41	1.51
17	V	301	3BV	C13-C14	-3.41	1.42	1.51
17	H	301	3BV	C13-C14	-3.35	1.42	1.51
17	H	301	3BV	C51-C47	3.30	1.59	1.53
17	V	301	3BV	C51-C47	3.30	1.59	1.53
17	N	201	3BV	C59-C51	3.11	1.56	1.52
17	b	201	3BV	C59-C51	2.71	1.55	1.52

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	301	3BV	C43-C42-N41	-6.33	102.07	110.20
17	V	301	3BV	C43-C42-N41	-6.17	102.27	110.20
17	b	201	3BV	C43-C42-N41	-5.19	103.54	110.20
17	N	201	3BV	C43-C42-N41	-5.02	103.76	110.20
17	b	201	3BV	C58-C51-C59	-5.01	103.38	109.76
17	N	201	3BV	C58-C51-C59	-4.94	103.47	109.76
17	H	301	3BV	O1-C6-C5	-3.62	103.98	111.77
17	V	301	3BV	C2-C3-N4	-3.62	104.63	110.12
17	V	301	3BV	O1-C6-C5	-3.59	104.04	111.77
17	H	301	3BV	C2-C3-N4	-3.46	104.86	110.12
17	H	301	3BV	C13-C12-C11	-3.43	106.27	113.21
17	V	301	3BV	C13-C12-C11	-3.43	106.28	113.21
17	H	301	3BV	C33-C32-C31	-3.38	104.36	113.36
17	V	301	3BV	C33-C32-C31	-3.38	104.38	113.36
17	N	201	3BV	O1-C6-C5	-3.26	104.74	111.77
17	b	201	3BV	O1-C6-C5	-3.24	104.80	111.77
17	b	201	3BV	C43-C42-C47	-3.10	107.23	112.18
17	V	301	3BV	C25-C24-C23	-3.09	107.12	115.40
17	H	301	3BV	C25-C24-C23	-3.09	107.12	115.40
17	N	201	3BV	C43-C42-C47	-3.04	107.31	112.18
17	N	201	3BV	O1-C2-C3	-2.97	105.37	111.77
17	b	201	3BV	C33-C32-C31	-2.93	105.56	113.36
17	b	201	3BV	O1-C2-C3	-2.92	105.48	111.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	3BV	C33-C32-C31	-2.84	105.81	113.36
17	V	301	3BV	O1-C2-C3	-2.73	105.88	111.77
17	H	301	3BV	O1-C2-C3	-2.70	105.95	111.77
17	b	201	3BV	C12-C13-C14	-2.70	104.34	113.22
17	N	201	3BV	C12-C13-C14	-2.67	104.42	113.22
17	b	201	3BV	C12-C11-C20	-2.60	103.77	110.11
17	N	201	3BV	C12-C11-C20	-2.53	103.93	110.11
17	V	301	3BV	C6-C5-N4	-2.53	106.28	110.12
17	H	301	3BV	C6-C5-N4	-2.47	106.36	110.12
18	V	302	MES	O1S-S-C8	2.40	110.36	106.73
18	H	302	MES	O2S-S-C8	2.40	110.35	106.73
17	V	301	3BV	C7-N4-C5	2.36	114.82	111.14
17	H	301	3BV	C7-N4-C5	2.36	114.82	111.14
17	b	201	3BV	C24-C23-N22	2.30	115.78	110.58
17	N	201	3BV	C24-C23-N22	2.25	115.66	110.58
17	H	301	3BV	C7-N4-C3	2.14	114.47	111.14
18	V	302	MES	O3S-S-C8	2.08	110.08	106.00
17	V	301	3BV	C7-N4-C3	2.05	114.34	111.14

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	H	301	3BV	C47-C42-C43-C44
17	N	201	3BV	C47-C42-C43-C44
17	N	201	3BV	C42-C47-C51-C58
17	N	201	3BV	C42-C47-C51-C59
17	V	301	3BV	C47-C42-C43-C44
17	b	201	3BV	C47-C42-C43-C44
17	b	201	3BV	C42-C47-C51-C58
17	b	201	3BV	C42-C47-C51-C59
18	H	302	MES	C7-C8-S-O1S
17	H	301	3BV	C20-C11-C12-C13
17	V	301	3BV	C20-C11-C12-C13
17	H	301	3BV	N10-C11-C12-C13
17	V	301	3BV	N10-C11-C12-C13
17	N	201	3BV	O48-C47-C51-C58
17	b	201	3BV	O48-C47-C51-C58
18	H	302	MES	C7-C8-S-O3S
17	N	201	3BV	O48-C47-C51-C59
17	b	201	3BV	O48-C47-C51-C59
18	H	302	MES	C8-C7-N4-C3

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Mol	Chain	Res	Type	Atoms
18	H	302	MES	C8-C7-N4-C5
18	V	302	MES	C8-C7-N4-C5
17	N	201	3BV	N22-C23-C24-C25
17	b	201	3BV	N22-C23-C24-C25
17	b	201	3BV	N4-C7-C8-N10
17	H	301	3BV	N41-C42-C43-C44
17	N	201	3BV	N41-C42-C43-C44
17	V	301	3BV	N41-C42-C43-C44
17	b	201	3BV	N41-C42-C43-C44
17	N	201	3BV	N4-C7-C8-N10
17	N	201	3BV	N4-C7-C8-O9
17	b	201	3BV	N4-C7-C8-O9
18	H	302	MES	C7-C8-S-O2S
18	V	302	MES	C8-C7-N4-C3
17	N	201	3BV	N10-C11-C20-N22
17	b	201	3BV	N10-C11-C20-N22
17	N	201	3BV	C8-C7-N4-C5
17	N	201	3BV	C8-C7-N4-C3
17	b	201	3BV	C8-C7-N4-C5
17	b	201	3BV	C8-C7-N4-C3
17	N	201	3BV	N10-C11-C20-O21
17	b	201	3BV	N10-C11-C20-O21
17	N	201	3BV	N30-C31-C32-C33
17	b	201	3BV	N30-C31-C32-C33

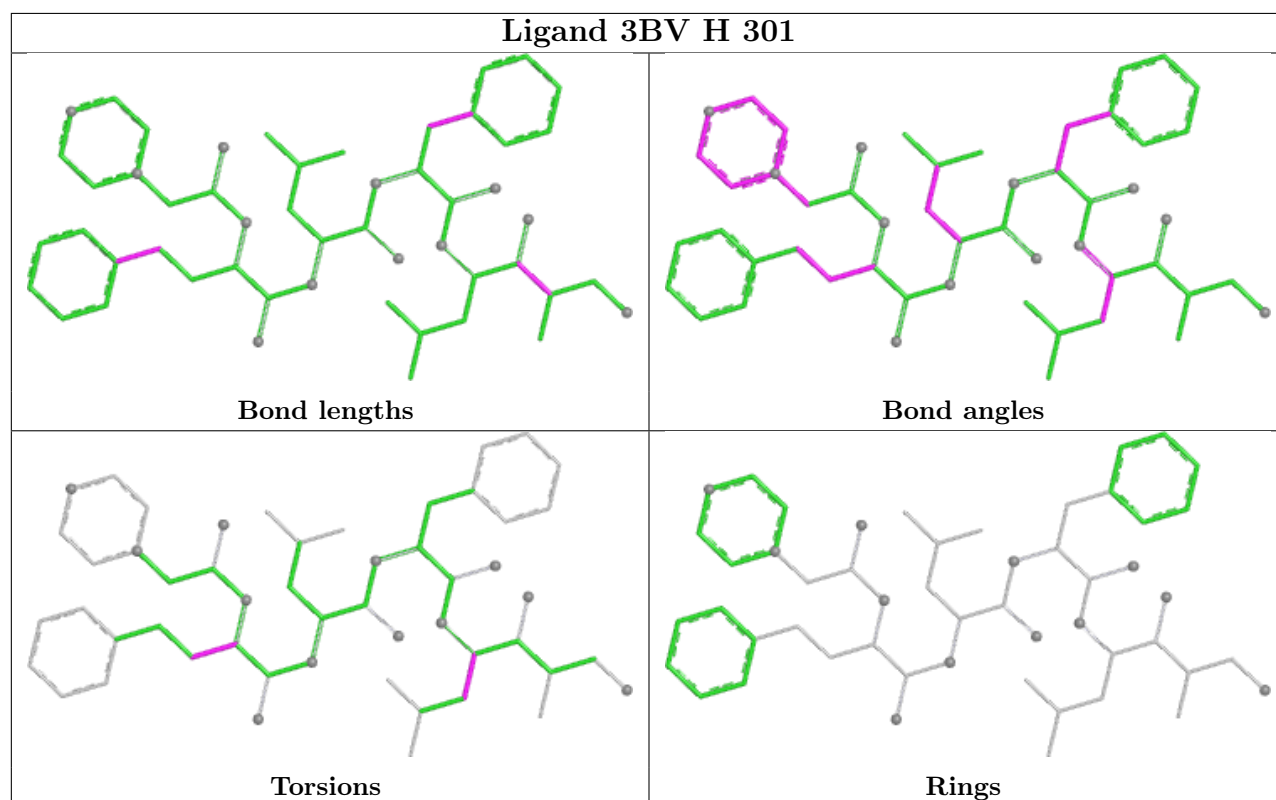
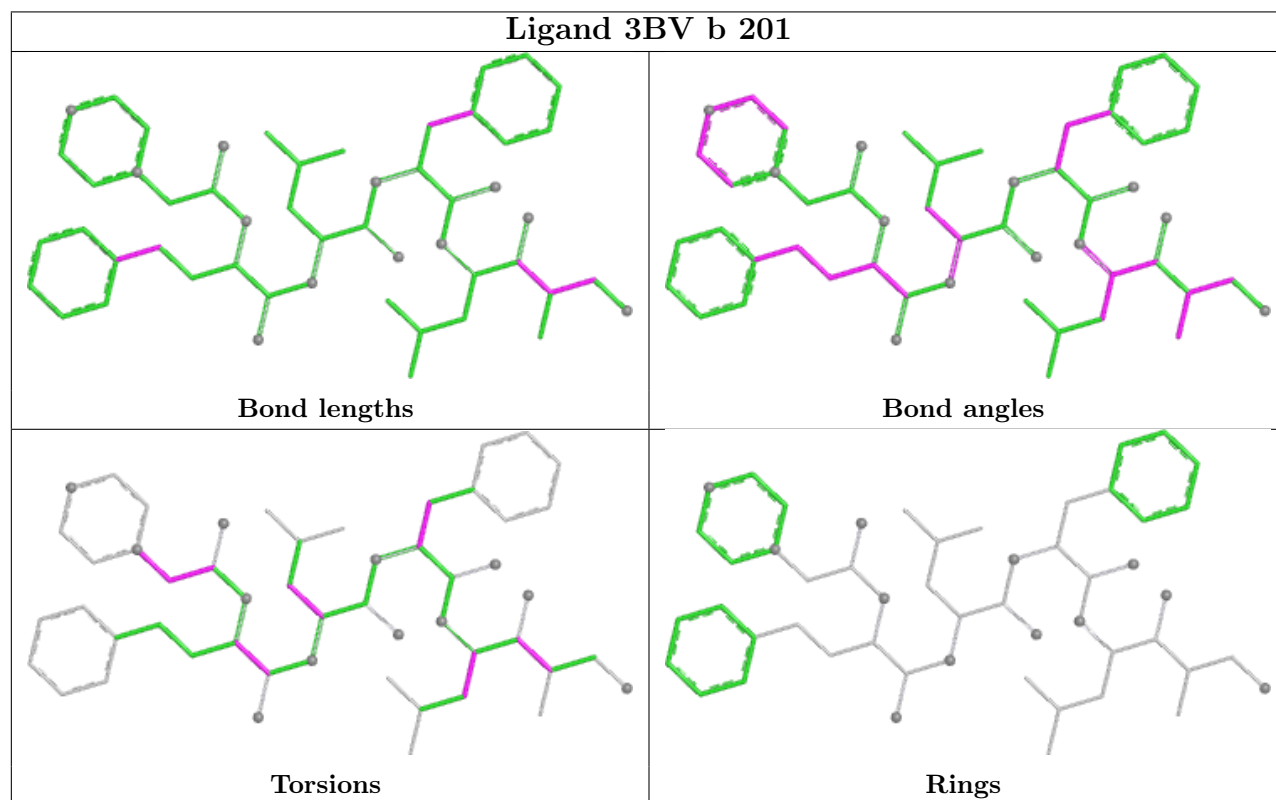
There are no ring outliers.

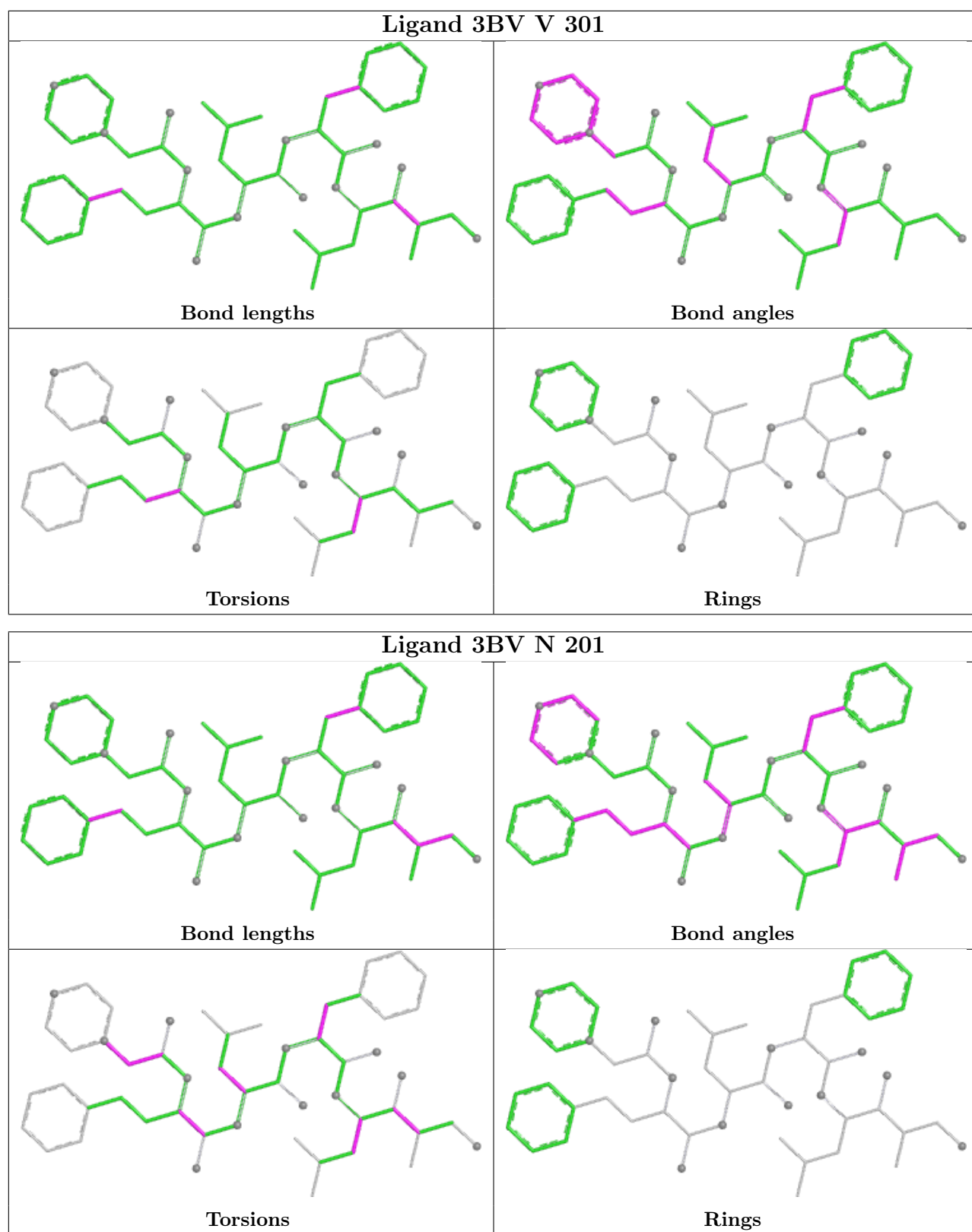
4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	b	201	3BV	1	0
17	H	301	3BV	3	0
17	V	301	3BV	3	0
17	N	201	3BV	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	0:GLY	C	1:CYS	N	5.36

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.36	2 (0%) 82 77	42, 58, 95, 149	0
1	O	250/250 (100%)	-0.26	2 (0%) 82 77	46, 66, 111, 149	0
2	B	244/258 (94%)	-0.17	2 (0%) 82 77	40, 64, 114, 166	0
2	P	244/258 (94%)	-0.14	4 (1%) 70 62	45, 70, 116, 168	0
3	C	240/254 (94%)	-0.13	3 (1%) 75 67	43, 70, 139, 171	0
3	Q	240/254 (94%)	0.01	7 (2%) 53 45	53, 83, 162, 185	0
4	D	235/260 (90%)	-0.08	2 (0%) 81 75	53, 75, 108, 145	0
4	R	235/260 (90%)	-0.00	3 (1%) 75 67	60, 79, 121, 164	0
5	E	231/234 (98%)	-0.05	0 100 100	51, 78, 115, 152	0
5	S	231/234 (98%)	0.12	3 (1%) 75 67	51, 83, 131, 169	0
6	F	243/288 (84%)	-0.19	1 (0%) 88 85	46, 69, 116, 149	0
6	T	243/288 (84%)	0.08	7 (2%) 53 45	51, 78, 136, 174	0
7	G	241/252 (95%)	-0.33	0 100 100	39, 58, 99, 151	0
7	U	241/252 (95%)	-0.28	1 (0%) 88 85	39, 62, 96, 139	0
8	H	222/232 (95%)	-0.34	0 100 100	36, 53, 92, 116	0
8	V	222/232 (95%)	-0.37	0 100 100	36, 56, 89, 124	0
9	I	204/205 (99%)	-0.51	1 (0%) 87 83	37, 54, 83, 110	0
9	W	204/205 (99%)	-0.48	0 100 100	37, 57, 84, 118	0
10	J	195/198 (98%)	-0.38	1 (0%) 87 83	38, 57, 88, 123	0
10	X	195/198 (98%)	-0.34	3 (1%) 72 64	42, 61, 91, 149	0
11	K	218/218 (100%)	-0.05	3 (1%) 73 65	44, 65, 98, 114	0
11	Y	212/218 (97%)	-0.16	3 (1%) 73 65	46, 63, 95, 115	0
12	L	222/222 (100%)	-0.33	1 (0%) 87 83	31, 60, 100, 130	0
12	Z	222/222 (100%)	-0.32	0 100 100	37, 58, 101, 128	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.41	1 (0%) 88 85	36, 57, 82, 92	0
13	a	233/246 (94%)	-0.40	2 (0%) 81 75	35, 55, 79, 90	0
14	N	196/196 (100%)	-0.46	0 100 100	32, 51, 82, 109	0
14	b	196/196 (100%)	-0.42	0 100 100	37, 52, 85, 107	0
All	All	6342/6626 (95%)	-0.23	52 (0%) 82 77	31, 64, 113, 185	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	X	1	MET	5.5
11	K	0	GLY	5.2
10	J	1	MET	4.6
1	A	1	MET	4.5
13	a	1	THR	4.2
3	Q	50	LEU	3.7
4	R	241	ALA	3.5
12	L	163	GLY	3.5
11	K	-5	ILE	3.4
3	Q	49	THR	3.4
1	O	1	MET	3.3
3	Q	205	ALA	3.2
13	M	1	THR	3.1
2	P	218	GLY	3.0
7	U	2	GLY	3.0
11	Y	209	ASN	3.0
2	B	218	GLY	3.0
6	T	243	ILE	2.9
2	P	219	ALA	2.8
11	K	209	ASN	2.8
6	T	14	ASP	2.8
2	P	51	VAL	2.7
4	D	240	ALA	2.7
6	T	241	LYS	2.7
6	T	53	LYS	2.6
4	R	230	GLU	2.6
11	Y	208	ASN	2.5
3	Q	234	ILE	2.4
6	F	243	ILE	2.4
3	C	204	GLY	2.3
5	S	209	ASN	2.3
5	S	52	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
13	a	69	ASP	2.3
3	C	205	ALA	2.3
4	R	113	LEU	2.3
9	I	1	SER	2.3
2	B	219	ALA	2.2
5	S	122	TYR	2.2
3	Q	204	GLY	2.2
6	T	204	LYS	2.2
11	Y	116	ASP	2.2
3	Q	238	LYS	2.2
1	O	249	ALA	2.2
6	T	178	HIS	2.1
6	T	201	GLU	2.1
2	P	58	GLN	2.1
10	X	139	TYR	2.1
4	D	241	ALA	2.1
1	A	201	GLU	2.1
3	Q	51	LYS	2.0
3	C	49	THR	2.0
10	X	194	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	MG	H	303	1/1	0.85	0.19	38,38,38,38	0
17	3BV	N	201	52/52	0.86	0.14	37,52,131,135	0
18	MES	V	302	12/12	0.86	0.17	64,68,101,103	0

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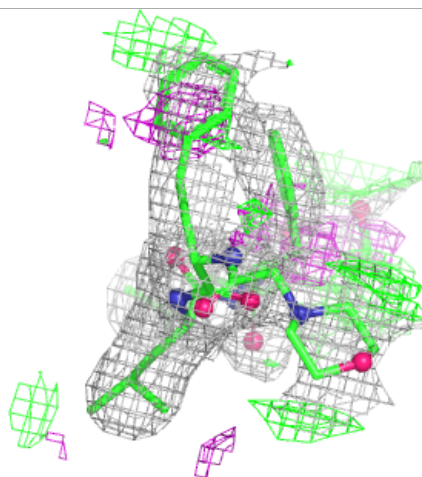
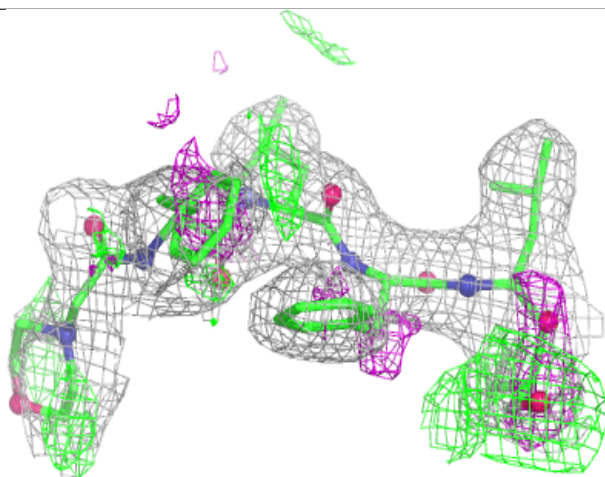
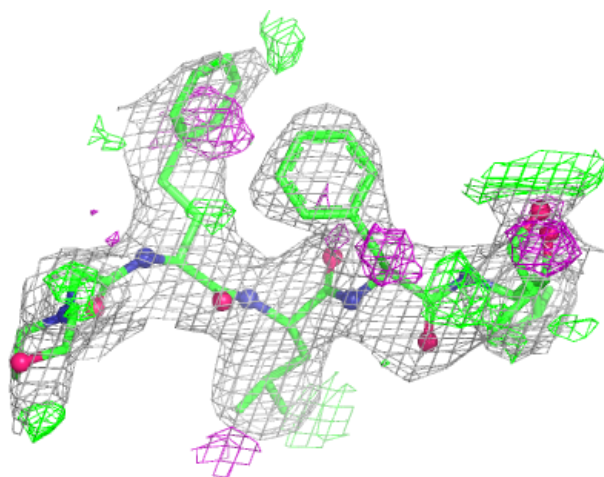
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
17	3BV	b	201	52/52	0.88	0.12	40,53,130,133	0
17	3BV	V	301	52/52	0.92	0.11	47,52,102,107	0
18	MES	H	302	12/12	0.93	0.14	60,65,71,79	0
17	3BV	H	301	52/52	0.93	0.11	44,51,97,102	0
15	MG	L	301	1/1	0.94	0.12	69,69,69,69	0
15	MG	Z	301	1/1	0.95	0.07	61,61,61,61	0
15	MG	K	301	1/1	0.96	0.07	58,58,58,58	0
15	MG	G	301	1/1	0.98	0.06	54,54,54,54	0
15	MG	I	301	1/1	0.98	0.09	58,58,58,58	0
15	MG	I	302	1/1	0.98	0.07	59,59,59,59	0
16	CL	N	203	1/1	0.98	0.04	44,44,44,44	0
16	CL	U	301	1/1	0.98	0.09	49,49,49,49	0
16	CL	b	202	1/1	0.98	0.07	50,50,50,50	0
16	CL	G	302	1/1	0.99	0.04	48,48,48,48	0
15	MG	N	202	1/1	0.99	0.03	41,41,41,41	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

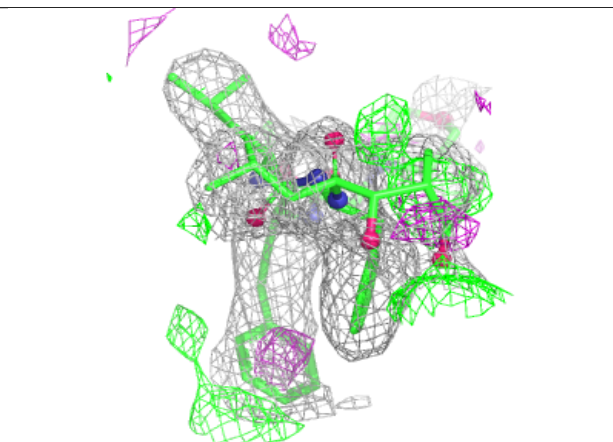
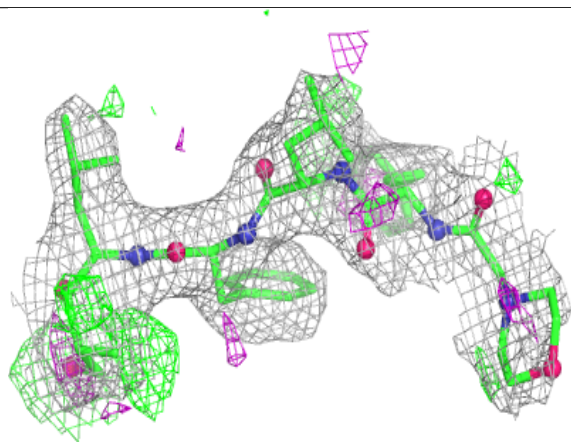
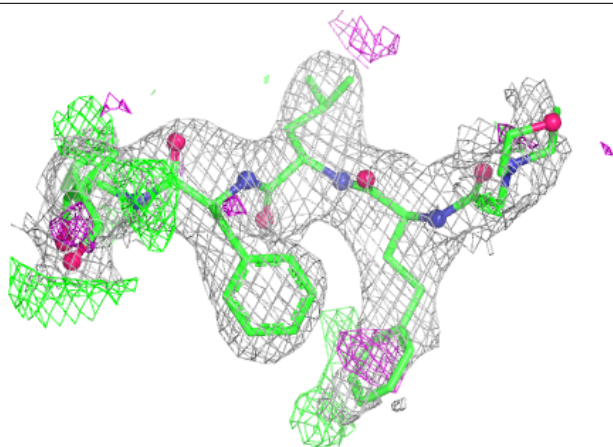
Electron density around 3BV N 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

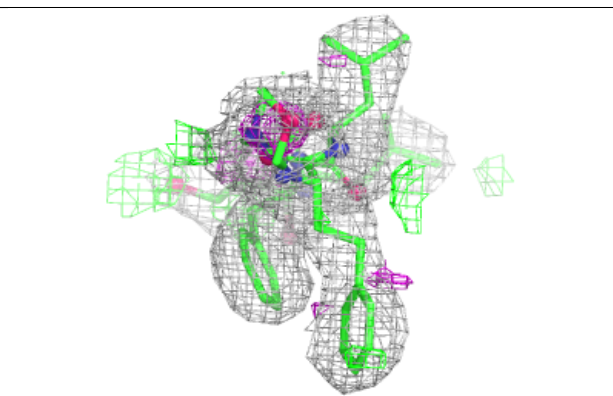
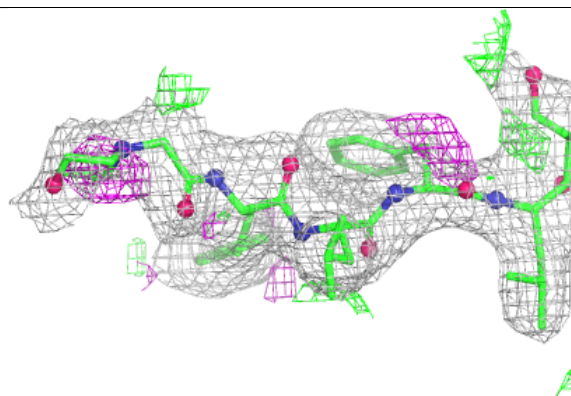
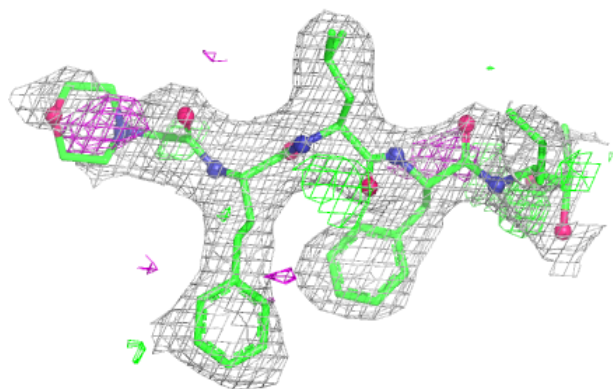


Electron density around 3BV b 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

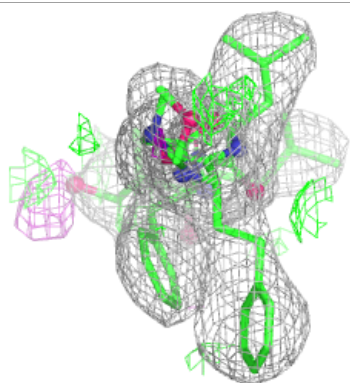
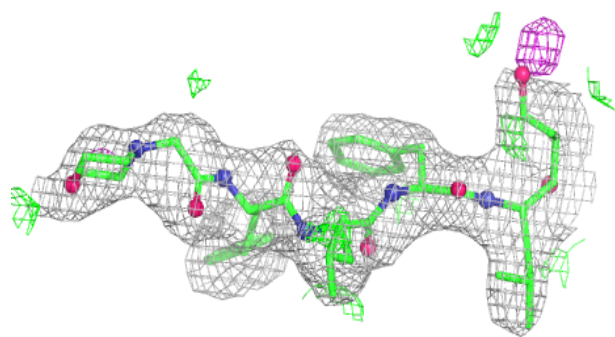
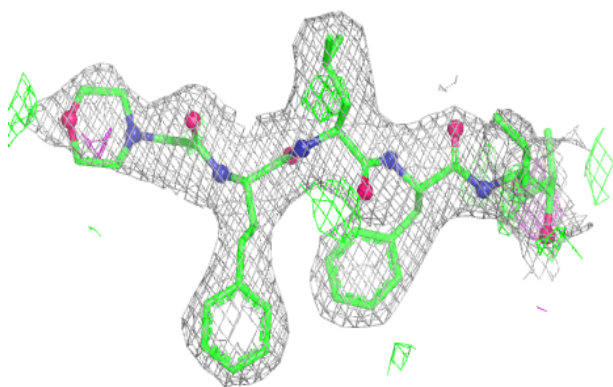
**Electron density around 3BV V 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 3BV H 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.